Cell Stem Cell
Forum

A Call for Standardized Naming and Reporting of Human ESC and iPSC Lines

Mai X. Luong,[1,*] Jonathan Auerbach,[2] Jeremy M. Crook,[3] Laurence Daheron,[4] Derek Hei,[5] Geoffrey Lomax,[6] Jeanne F. Loring,[7] Tenneille Ludwig,[8] Thorsten M. Schlaeger,[9] Kelly P. Smith,[1] Glyn Stacey,[10] Ren-He Xu,[11] and Fanyi Zeng[12]
[1]International Stem Cell Registry, Department of Cell Biology, University of Massachusetts Medical School, Shrewsbury, MA 01545, USA
[2]GlobalStem, Rockville, MD 20850, USA
[3]Stem Cell Medicine, O'Brien Institute and Department of Surgery, St. Vincent's Hospital, The University of Melbourne, Melbourne, VIC 3065, Australia
[4]Harvard iPSC Core Facility, Cambridge, MA 02138, USA
[5]Waisman Clinical Biomanufacturing Facility, Madison, WI 53705, USA
[6]California Institute for Regenerative Medicine (CIRM), San Francisco, CA 94107, USA
[7]Center for Regenerative Medicine, The Scripps Research Institute, La Jolla, CA 92037, USA
[8]WiCell Research Institute (WISC Bank), Madison, WI 53705, USA
[9]Children's Hospital Boston Human Embryonic Stem Cell Core Facility, Boston, MA 02115, USA
[10]UK Stem Cell Bank, National Institute for Biological Standards and Control-HPA, Herts, EN63QG, UK
[11]University of Connecticut Health Center, Farmington, CT 06030, USA
[12]Shanghai Jiao Tong University, Shanghai, China
*Correspondence: mai.luong@umassmed.edu
DOI 10.1016/j.stem.2011.03.002

Human embryonic and induced pluripotent stem cell lines are being generated at a rapid pace and now number in the thousands. We propose a standard nomenclature and suggest the use of a centralized database for all cell line names and a minimum set of information for reporting new derivations.

Stem cell research would benefit from precise cell line identification by standardized nomenclature and minimum standards for reporting cell line provenance, derivation, culture, and characterization. To date, confusion has arisen from multiple names being applied to individual human embryonic stem cell (ESC) and induced pluripotent stem cell (iPSC) lines, as well as use of the same name for different cell lines. In addition, publications of methods for deriving, culturing, and characterizing cell lines do not always provide sufficient information to permit the repetition or thorough assessment of the work. To address these issues, we have devised a proposal for a standard nomenclature for human iPSC and ESC lines and a suggestion for a minimum set of criteria for reporting new cell lines. Furthermore, we propose that it would be helpful to establish a centralized database for all cell line names. This article is the culmination of workshops held at the International Society for Stem Cell Research (ISSCR) satellite symposium on Stem Cell Facilities and Resources on June 15, 2010 and the International Stem Cell Initiative (ISCI) meeting on September 15, 2010.

Naming of Cell Lines

The current lack of a naming convention for human ESC and iPSC lines has resulted in a broad spectrum of names ranging from a single number to many and varied combinations of letters, numbers, and hyphens (e.g., "60" and "DH1CF32-IPS2") (Woltjen et al., 2009; Park et al., 2008). Furthermore, cell line names are not used consistently in different publications and sometimes not even within the same publication. These inconsistencies make literature searches difficult, as a whole body of work may be missed because of a different placement of a hyphen or inconsistent inclusion of a zero (e.g., "ABC2," "ABC 2," "ABC-2" or "XYZ3," "XYZ03," "XYZ003"). Inconsistent naming makes it difficult to accurately count existing cell lines and can cause confusion about the identity of certain cell lines.

In the absence of a standardized system for unique naming and reporting cell lines, duplication of names is inevitable and problematic. For example, two iPSC lines derived from amniotic fluid (AF) samples are named "AF-iPS" even though they are from different patients in separate studies (Ye et al., 2009; Galende et al., 2010). Other examples include lines named "DMD-iPS1" that are generated from two Duchenne Muscular Dystrophy patients with different mutations in the dystrophin gene (Park et al., 2008; Kazuki et al., 2010). Lastly, more simplistic names such as "iPS-1" and "iPS-WT" have also been duplicated (Lowry et al., 2008; Zhou and Freed, 2009).

Ambiguity about cell line identity is likely to hamper evaluation of the validity and reproducibility of research findings. While we do not advocate the renaming of existing cell lines, the adoption of a convention for naming new human ESC and iPSC cell lines is advisable and recommended based on the combined workshop discussions. Scientific nomenclatures currently in use range from the

Table 1. Advantages of Proposed Nomenclature

Unique identifier avoids confusion between cell lines
Intuitive naming strategy provides recognizable information about the cell lines
Similar format to many existing names (e.g., CT4, B124-2)
Easy to distinguish between different sets of lines (TSRI68i-YF versus SHEF4e-ALS), and different cell lines within a set (SHEF3 versus SHEF5)
Flexible and does not require a consensus on the types of information to be included

simple CD nomenclature (e.g., "CD8," "CD42a," "CD42b") to the extremely complex mouse strain and mutation nomenclature (e.g., "B6-*Apoa1*^{tm1Unc}/J"). We put forward a proposal for a hybrid naming system, drawing from accepted nomenclatures of other fields (Table 1).

Our proposed system contains four elements in the following order (Figure 1): a group of letters, a serial number, an "i" or "e" to represent "iPSC" or "ESC," and a descriptor that is preceded by a dash. The "i/e" and descriptor are optional. The group of letters would indicate the source, which could be an abbreviation for an institute or laboratory (e.g., "SHEF" or "HUES"). While the exact number of characters for any element can vary, we recommend that names have no spaces and be limited to 14 characters. However, it is strongly recommended that the shortest possible cell line names be used in order to avoid laborious labeling of cell culture dishes or cryotubes. In making these recommendations, we are not proposing to rename existing cell lines. The owner of the cell line could, of course, opt to change the name to the new format and inform registries.

Although the nomenclature proposal described in Figure 1 aims to standardize cell line naming, it will not completely prevent name duplication on its own, which minimally requires that investigators have access to a listing of all published cell lines. To address this issue, we envision that an online process that allows investigators to quickly submit all their cell line names to a centralized database, which has yet to be identified, will be an important asset to the field. We suggest an international committee be convened to discuss the implementation of this process. Establishment and adoption of a central database for all cell line names involve many challenges and would require support from journals and broad agreement from the stem cell field. However, we believe that such a database is the best possible solution to name duplication.

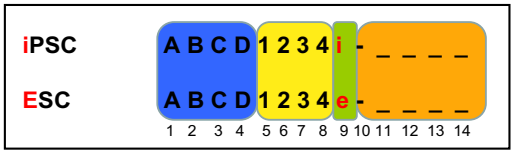

Figure 1. Proposed Nomenclature for Cell Line Names
Blue box: contains a group of letters to represent source reference, such as laboratory (for iPSC lines) or institution (for hESC lines). Yellow box: may contain a sequential number to identify specific cell lines. Green box: contains an "i" or "e" to represent "iPSC" or "ESC," respectively. Orange box: begins with a dash and is followed by up to 12 letters and/or numbers. This box can be used to note specific characteristics such as disease, reporter genes, patient number and clone number. The green and orange boxes are optional. Total number of characters (including dash) should be limited to 14.

Reporting Derivations

Traceability, interpretation, and repetition of reported human ESC and iPSC studies require clear communication of the systems used, the procedures followed, and the outcomes (Coecke et al., 2005). Traceability is especially important information for manuscripts concerning human pluripotent stem cell lines because multiple laws, regulations and guidelines govern the use of cell lines. Thus, we describe a proposed set of minimal information be included in reports of cell line derivation: provenance, source, derivation method, characterization, genetic identity, and sterility (Table 2). Important details to include are as follows: process of donor consent, whether the source or starting material is patient-derived or obtained from a cell bank, an accession number if the cell source is commercially available, method used for embryo handling and isolation of inner cell mass for human ESCs or reprogramming for iPSCs, characterization of the undifferentiated state and demonstration of pluripotency, cell line verification by identity profile, and mycoplasma testing (International Stem Cell Banking Initiative, 2009).

Conclusion

In summary, we advocate standardized reporting, naming, and listing of human ESC and iPSC lines at a centralized database to facilitate effective and accurate evaluation and application of research using these cell lines. Our recommendations have been developed through consultation with a large, although still incomplete, subset of the international stem cell community and have been approved by the Steering Committee of the International Stem Cell Initiative. Thus discussions are ongoing and will likely require further debate and input from the field.

Table 2. Recommended Minimal Set of Information for Publishing New Lines

Source	Derivation Method	Characterization	Genetic Identity and Sterility	Provenance
Patient-derived or cell bank	hESC (e.g., zona pellucida removal, cell isolation and seeding, culture conditions)	undifferentiated state (e.g., immunocytochemistry, FACS, molecular profiling)	identity profile (e.g., STR, SNP): not necessarily published fully, but held for matching.	consent (statement about consenting process and evidence of human subjects oversight)
Cell type, tissue source and passage number	reprogramming method (e.g., vector system, small molecules, protein, mRNA, or miRNA transduction/transfection)	pluripotency (e.g., in vitro differentiation, teratoma assay, molecular profiling)	mycoplasma (recommended routine practice, include specific test used)	conflict of interest disclosure
Age (a range, if specific age cannot be disclosed)		genetic characterization (e.g., karyotype, SNP genotype)		
Ethnicity (self-reported and/or determined by analysis)		disease history, if applicable		

ACKNOWLEDGMENTS

We are grateful for the support of this workshop at the annual ISCI meeting that was funded by the International Stem Cell Forum. We would also like to thank the ISSCR for providing a venue for this nomenclature discussion. In addition, the authors would like to thank the following organizations for their support: the Massachusetts Life Sciences Center (M.X.L. and K.P.S.), the Helen Macpherson Smith Trust (J.M.C.), CIRM, NIH, Esther O'Keefe Foundation, and Millipore Foundation (J.F.L.).

REFERENCES

Coecke, S., Balls, M., Bowe, G., Davis, J., Gstraunthaler, G., Hartung, T., Hay, R., Merten, O.W., Price, A., Schechtman, L., et al; Second ECVAM Task Force on Good Cell Culture Practice. (2005). Altern. Lab. Anim. *33*, 261–287.

Galende, E., Karakikes, I., Edelmann, L., Desnick, R.J., Kerenyi, T., Khouiery, G., Lafferty, J., McGinn, J.T., Brodman, M., Fuster, V., et al. (2010). Cell Reprogram. *12*, 117–125.

Kazuki, Y., Hiratsuka, M., Takiguchi, M., Osaki, M., Kajitani, N., Hoshiya, H., Hiramatsu, K., Yoshino, T., Kazuki, Ishihara, C., et al. (2010). Mol. Ther. *18*, 386–393.

International Stem Cell Banking Initiative. (2009). Stem Cell Rev. *5*, 301–314.

Lowry, W.E., Richter, L., Yachechko, R., Pyle, A.D., Tchieu, J., Sridharan, R., Clark, A.T., and Plath, K. (2008). Proc. Natl. Acad. Sci. USA *105*, 2883–2888.

Park, I.H., Arora, N., Huo, H., Maherali, N., Ahfeldt, T., Shimamura, A., Lensch, M.W., Cowan, C., Hochedlinger, K., and Daley, G.Q. (2008). Cell *134*, 877–886.

Woltjen, K., Michael, I.P., Mohseni, P., Desai, R., Mileikovsky, M., Hämäläinen, R., Cowling, R., Wang, W., Liu, P., Gertenstein, M., et al. (2009). Nature *458*, 766–770.

Ye, L., Chang, J.C., Lin, C., Sun, X., Yu, J., and Kan, Y.W. (2009). Proc. Natl. Acad. Sci. USA *106*, 9826–9830.

Zhou, W., and Freed, C.R. (2009). Stem Cells *27*, 2667–2674.